Amendments to the Specification:

Please replace the paragraph beginning at page 7, line 11, with the following:

--**Figure 1.** Amino acid alignment of CNG3B (SEQ ID NO:13) with human CNGA1 (SEQ ID NO:14) and CNGA3 (SEQ ID NO:15). Identical residues are shaded and numbers at the left margin indicate amino acid position.--

Please replace the paragraph beginning at page 7, line 14, with the following:

--**Figure 2.** Complete CNG3B sequence (SEQ ID NO:16) derived from assembly of PCR fragments. ~~Coding sequence is in bold type, and untranslated sequence is in normal type.~~--

Please replace the paragraph beginning at page 7, line 17, with the following:

--**Figure 3.** Complete CNG3B coding nucleotide sequence (SEQ ID NO:3).--

Please replace the paragraph beginning at page 7, line 18, with the following:

--**Figure 4.** Complete CNG3B amino acid sequence (SEQ ID NO:1).--

Please replace the paragraph beginning at page 11, line 19, with the following:

--"CNG3B" refers to a polypeptide that is a subunit or monomer of a cyclic nucleotide gated cation channel, and a member of the CNG family. When CNG3B is part of a

cation channel, e.g., a heteromeric cation channel, the channel has the characteristic of cyclic nucleotide gating. The term CNG3B therefore refers to CNG3B polymorphic variants, alleles, mutants, and interspecies homologs that: (1) have a subsequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, preferably 85%, 90%, or 95% amino acid sequence identity, to the CNG3B conserved region (amino acids 210-661 of SEQ ID NO:1), or, optimally, comprise 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or greater identity to a CNG3B amino acid sequence of SEQ ID NO:1; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence of SEQ ID NO:1 or amino acids 210-661 of SEQ ID NO:1, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a sequence of SEQ ID NOS:2-3 or a nucleotide sequence encoding amino acids 210-661 of SEQ ID NO:1, and conservatively modified variants thereof; or (4) are amplified by primers that specifically hybridize under stringent hybridization conditions to the same sequence as a primer set selected from the group consisting of ~~SEQ ID NOS:6-13~~ SEQ ID NOS:4-12.--

Please replace the paragraph beginning at page 61, line 17, with the following:

--An approximately 180 bp band from the middle of CNG3B was amplified from human cDNAs prepared from the retina, demonstrating expression in this tissue. The oligos used to amplify this band were 5'-(1) TCTATCTCCTGTGGCTCTTGCTTGTC (SEQ ID NO:4) (sense) and 5'-(2) GAGTCTGGGCTGGATAAATAGCATATC (SEQ ID NO:5) (antisense). An approximately 787 bp band from the middle of CNG3B was amplified from human retina using 5'-(3) AGGAATTGGCACTACTAGATGGGTG (SEQ ID NO:6) (sense) and 5'-(4) TTCATGAGGATCCTTTCAGAATCTGG (SEQ ID NO:7) (antisense) oligos. An approximately 1.26 kb band from the middle of CNG3B was amplified from human retina using 5'-(1) TCTATCTCCTGTGGCTCTTGCTTGTC (SEQ ID NO:4) (sense) and 5'-(4) TTCATGAGGATCCTTTCAGAATCTGG (SEQ ID NO:7) (antisense) oligos. The 1.26 kb fragment (5'-1 & 4) was subcloned and its sequence confirmed.--

Please replace the paragraph beginning at page 61, line 29, with the following:

--The complete 3' end of CNG3B was amplified by standard 3' RACE PCR techniques from human retina cDNA in two successive rounds. In the first round the gene specific primer used was 5'- (5) GGAAACCGTCGAACTGCCAATGTGGT (SEQ ID NO:8) (sense). This reaction was reamplified with a nested gene specific oligo 5'-(6) CGGGTTTGCCAATCTTTTAACTCTAGAC (SEQ ID NO:9) (sense) which produced a band approximately 810 bp in length that, when sequenced, was found to include the complete 3' end of the CNG3B mRNA. This fragment overlapped with the original 1.26 kb CNG3B fragment to provide contiguous sequence. The 5' end of CNG3B was amplified from human retina cDNA using two rounds of standard 5' RACE PCR. The oligo 5'-(2) GAGTCTGGGCTGGATAAATAGCATATC (SEQ ID NO:5) (antisense) was used in the first round of RACE PCR and reamplified using the nested gene specific oligo 5'-(7) GTCCGCAATAAGCCAGTAGTGTATG (SEQ ID NO:10) (antisense). An approximately 830 bp fragment containing the complete 5' end of CNG3B including the start codon (Methionine) was isolated. This fragment also overlapped the original 1.26 kb fragment allowing us to determine the entire contiguous coding region of the CNG3B mRNA using both the 5' & 3' RACE products with the original 1.26 kb sequence.--

Please replace the paragraph beginning at page 62, line 12, with the following:

--The entire coding region of CNG3B was then isolated in a single fragment using oligonucleotides overlapping the CNG3B coding sequence ends as determined from sequence analysis of the above fragments. The oligonucleotides used were 5'-(8) TGACAAGCTTCCGCC**ATGTTTAAATCGCTGACAAAAGTC** (SEQ ID NO:11) (sense) and 5'-(9) TGACGAATTC**TCCCAGCATGTCGTTTCCCCTCGTTAA** (SEQ ID NO:12) (antisense). The first oligonucleotide includes the initiator methionine, the first 24 coding nucleotides of the CNG3B gene, and, upstream, a HindIII restriction enzyme site for subcloning

into plasmid vectors and a Kozak consensus sequence to boost translation. All nucleotides corresponding to CNG3B are in bold type. The second oligonucleotide is from the 3' untranslated sequence of CNG3B and includes an EcoRI restriction enzyme site for subcloning. Again, all nucleotides in bold correspond to the untranslated region of the 3' end of CNG3B (*i.e.*, the only nucleotides required for the amplification of CNG3B are those in bold type from the two oligos above). The amplification conditions used were as follows: 24 cycles of 95°C for 15 seconds, 70-58°C for 15 seconds (temperature was dropped 0.5°C each successive cycle), 72°C for 2.5 minutes, followed by 16 cycles of 95°C for 15 seconds, 58°C for 15 seconds, and 72°C for 2.5 minutes. An approximately 2.51 kb band corresponding to the entire coding region of CNG3B was obtained and confirmed by sequencing.--

Please insert the accompanying paper copy of the Sequence Listing, page numbers 1 to 16, at the end of the application.